A Proteomic Approach for Plasma Biomarker Discovery with iTRAQ Labelling and OFFGEL Fractionation

Titre	A Proteomic Approach for Plasma Biomarker Discovery with iTRAQ Labelling and OFFGEL Fractionation
Type de publication	Article de revue
Auteur	Ernoult, Emilie [1], Bourreau, Anthony [2], Gamelin, Erick [3], Guette, Catherine [4]
Editeur	Hindawi Publishing Corporation
Type	Article scientifique dans une revue à comité de lecture
Année	2009
Langue	Anglais
Date	2009/11/01
Volume	2010
Titre de la revue	BioMed Research International
ISSN	2314-6133
Résumé en anglais	Human blood plasma contains a plethora of proteins, encompassing not only proteins that have plasma-based functionalities, but also possibly every other form of low concentrated human proteins. As it circulates through the tissues, the plasma picks up proteins that are released from their origin due to physiological events such as tissue remodeling and cell death. Specific disease processes or tumors are often characterized by plasma “signatures,” which may become obvious via changes in the plasma proteome profile, for example, through over expression of proteins. However, the wide dynamic range of proteins present in plasma makes their analysis very challenging, because high-abundance proteins tend to mask those of lower abundance. In the present study, we used a strategy combining iTRAQ as a reagent which improved the peptide ionization and peptide OFFGEL fractionation that has already been shown, in our previous research, to improve the proteome coverage of cellular extracts. Two prefractioning methods were compared: immunodepletion and a bead-based library of combinatorial hexapeptide technology. Our data suggested that both methods were complementary, with regard to the number of identified proteins. iTRAQ labelling, in association with OFFGEL fractionation, allowed more than 300 different proteins to be characterized from 400 microgramme of plasma proteins.
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DOI	10.1155/2010/927917 [6]
Lien vers le document	http://dx.doi.org/10.1155/2010/927917 [6]

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